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Raw Sequence Listing Error Summary

#4

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/434,208

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING

PATENT APPLICATION US/09/434,708

 DATE: 11/18/1999
 TIME: 14:43:39

Input Set: I434708.RAW

This Raw Listing contains the General Information
 Section and up to first 5 pages.

Does Not Comply
 Corrected Diskette Needed

1 <110> APPLICANT: Borriello, Francescopaolo
 2 Band, Hamid
 3 <120> TITLE OF INVENTION: Characterization of a novel gene Cbl-SL
 4 <130> FILE REFERENCE: B0801/7159/ERP
 5 <140> CURRENT APPLICATION NUMBER: US/09/434,708
 6 <141> CURRENT FILING DATE: 1999-11-05
 7 <150> EARLIER APPLICATION NUMBER: U.S. 60/107,470
 8 <151> EARLIER FILING DATE: 1998-11-06
 9 <160> NUMBER OF SEQ ID NOS: 10
 10 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 11 <210> SEQ ID NO 1
 12 <211> LENGTH: 1547
 13 <212> TYPE: DNA
 14 <213> ORGANISM: Homo Sapiens
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 16 <221> NAME/KEY: CDS
 17 <222> LOCATION: (13)...(1434)
 18 <400> SEQUENCE: 1
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 21 1 5 10
 22 gag gcc cgc gcc ctg ggc cgg gca gtc agg atg ctg cag cgc cta gaa 99
 23 Glu Ala Arg Ala Leu Gly Arg Ala Val Arg Met Leu Gln Arg Leu Glu
 24 15 20 25
 25 gag caa tgc gtc gac ccc cgg ctg tcc gtg agt ccc cct tcg ctg cgg 147
 26 Glu Gln Cys Val Asp Pro Arg Leu Ser Val Ser Pro Pro Ser Leu Arg
 27 30 35 40 45
 28 gac ctg ctg ccc cgc aca gcg cag ctg ctt cga gag gtg gcc cat tct 195
 29 Asp Leu Leu Pro Arg Thr Ala Gln Leu Leu Arg Glu Val Ala His Ser
 30 50 55 60
 31 cgg cgg gcg gcc ggc gga ggc ggc ccc ggg ggt ccc ggc ggc tct ggg 243
 32 Arg Arg Ala Ala Gly Gly Gly Gly Pro Gly Gly Pro Gly Gly Ser Gly
 33 65 70 75
 34 gac ttt cta ctc atc tac ctg gcc aat ctg gag gcc aag agc agg cag 291
 35 Asp Phe Leu Leu Ile Tyr Leu Ala Asn Leu Glu Ala Lys Ser Arg Gln
 36 80 85 90
 37 gtg gcc gcg ctg ctg cct ccc cgg ggc cga agg agt gcc aac gac gag 339
 38 Val Ala Ala Leu Leu Pro Pro Arg Gly Arg Arg Ser Ala Asn Asp Glu
 39 95 100 105
 40 ctc ttc cgg gcg ggc tcc aga ctc agg cga cag ctg gcc aag ctg gcc 387
 41 Leu Phe Arg Ala Gly Ser Arg Leu Arg Arg Gln Leu Ala Lys Leu Ala
 42 110 115 120 125
 43 atc atc ttc agc cac atg cac gca gag ctg cac gca ctc ttc ccc ggg 435
 44 Ile Ile Phe Ser His Met His Ala Glu Leu His Ala Leu Phe Pro Gly

45					130				135					140					
46	gca	aag	tac	tgt	gga	cac	atg	tac	cag	ctc	acc	aag	gcc	ccc	gcc	cac		483	
47	Ala	Lys	Tyr	Cys	Gly	His	Met	Tyr	Gln	Leu	Thr	Lys	Ala	Pro	Ala	His			
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49	acc	ttc	tgg	agg	gaa	agt	tgc	gga	gcc	cgg	tgt	gtg	ctg	ccc	tgg	gct		531	
50	Thr	Phe	Trp	Arg	Glu	Ser	Cys	Gly	Ala	Arg	Cys	Val	Leu	Pro	Trp	Ala			
51					160				165					170					
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53	Glu	Phe	Glu	Ser	Leu	Leu	Gly	Thr	Cys	His	Pro	Val	Glu	Pro	Gly	Cys			
54					175				180					185					
55	aca	gcc	ctg	gcc	ttg	cgc	acc	acc	att	gac	ctc	acc	tgc	agc	ggg	cac		627	
56	Thr	Ala	Leu	Ala	Leu	Arg	Thr	Thr	Ile	Asp	Leu	Thr	Cys	Ser	Gly	His			
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58	gtg	tcc	atc	ttc	gag	ttc	gac	gtc	ttc	acc	agg	ctc	ttt	cag	cca	tgg		675	
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61	cca	aca	ctc	ctc	aag	aac	tgg	cag	ctc	ctg	gca	gtc	aac	cac	cca	ggc		723	
62	Pro	Thr	Leu	Leu	Lys	Asn	Trp	Gln	Leu	Leu	Ala	Val	Asn	His	Pro	Gly			
63					225				230					235					
64	tac	atg	gcc	ttc	ctc	acc	tat	gat	gag	gtc	caa	gag	cgt	ctg	cag	gcc		771	
65	Tyr	Met	Ala	Phe	Leu	Thr	Tyr	Asp	Glu	Val	Gln	Glu	Arg	Leu	Gln	Ala			
66					240				245					250					
67	tgc	agg	gac	aag	cca	ggc	agt	tac	atc	ttc	cgg	ccc	agc	tgt	act	cgc		819	
68	Cys	Arg	Asp	Lys	Pro	Gly	Ser	Tyr	Ile	Phe	Arg	Pro	Ser	Cys	Thr	Arg			
69					255				260					265					
70	ctg	ggg	cag	tgg	gcc	atc	ggc	tat	gtg	agc	tca	gat	ggc	agc	atc	ctg		867	
71	Leu	Gly	Gln	Trp	Ala	Ile	Gly	Tyr	Val	Ser	Ser	Asp	Gly	Ser	Ile	Leu			
72					270				275					280					
73	cag	acc	atc	cct	gcc	aac	aaa	ccc	ctg	tcc	cag	gtg	ctc	ctg	gag	gga		915	
74	Gln	Thr	Ile	Pro	Ala	Asn	Lys	Pro	Leu	Ser	Gln	Val	Leu	Leu	Glu	Gly			
75					290				295					300					
76	cag	aag	gac	ggc	ttc	tac	ctc	tac	cca	gat	gga	aag	acc	cac	aac	cca		963	
77	Gln	Lys	Asp	Gly	Phe	Tyr	Leu	Tyr	Pro	Asp	Gly	Lys	Thr	His	Asn	Pro			
78					305				310					315					
79	gac	ctg	act	gag	ctc														

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/434,708

DATE: 11/18/1999
TIME: 14:43:39

Input Set: I434708.RAW

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98      Gly Asn Ser Ser Asp Gln Glu Gly Arg Glu Leu Glu Leu Gly Gln Val
99              415                      420                      425
100     ccc ctt tcg gct cct cca ttg ccc cca cgg cca gat ctg ccc ccc agg      1347
101     Pro Leu Ser Ala Pro Pro Leu Pro Pro Arg Pro Asp Leu Pro Pro Arg
102     430                      435                      440                      445
103     aag ccc aga aat gcc cag ccg aaa gtg aga ctc cta aag ggg aac tcc      1395
104     Lys Pro Arg Asn Ala Gln Pro Lys Val Arg Leu Leu Lys Gly Asn Ser
105              450                      455                      460
106     cct cca gct gcg ctg gga ccc cag gac cct gcc ccg gcc tgaaggccag      1444
107     Pro Pro Ala Ala Leu Gly Pro Gln Asp Pro Ala Pro Ala
108              465                      470
109     ggcacccaga tgtgctgctc aaggagcccc caagggctgg aagggggttg tgaaaccgaa      1504
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113     <212> TYPE: PRT
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119     20              25              30
120     Val Asp Pro Arg Leu Ser Val Ser Pro Pro Ser Leu Arg Asp Leu Leu
121     35              40              45
122     Pro Arg Thr Ala Gln Leu Leu Arg Glu Val Ala His Ser Arg Arg Ala
123     50              55              60
124     Ala Gly Gly Gly Gly Pro Gly Gly Pro Gly Gly Ser Gly Asp Phe Leu
125     65              70              75              80
126     Leu Ile Tyr Leu Ala Asn Leu Glu Ala Lys Ser Arg Gln Val Ala Ala
127     85              90              95
128     Leu Leu Pro Pro Arg Gly Arg Arg Ser Ala Asn Asp Glu Leu Phe Arg
129     100             105             110
130     Ala Gly Ser Arg Leu Arg Arg Gln Leu Ala Lys Leu Ala Ile Ile Phe
131     115             120             125
132     Ser His Met His Ala Glu Leu His Ala Leu Phe Pro Gly Ala Lys Tyr
133     130             135             140
134     Cys Gly His Met Tyr Gln Leu Thr Lys Ala Pro Ala His Thr Phe Trp
135     145             150             155             160
136     Arg Glu Ser Cys Gly Ala Arg Cys Val Leu Pro Trp Ala Glu Phe Glu
137     165             170             175
138     Ser Leu Leu Gly Thr Cys His Pro Val Glu Pro Gly Cys Thr Ala Leu
139     180             185             190
140     Ala Leu Arg Thr Thr Ile Asp Leu Thr Cys Ser Gly His Val Ser Ile
141     195             200             205
142     Phe Glu Phe Asp Val Phe Thr Arg Leu Phe Gln Pro Trp Pro Thr Leu
143     210             215             220
144     Leu Lys Asn Trp Gln Leu Leu Ala Val Asn His Pro Gly Tyr Met Ala

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145	225	230	235	240
146	Phe Leu Thr Tyr Asp Glu Val Gln Glu Arg Leu Gln Ala Cys Arg Asp			
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148	Lys Pro Gly Ser Tyr Ile Phe Arg Pro Ser Cys Thr Arg Leu Gly Gln			
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150	Trp Ala Ile Gly Tyr Val Ser Ser Asp Gly Ser Ile Leu Gln Thr Ile			
151		275	280	285
152	Pro Ala Asn Lys Pro Leu Ser Gln Val Leu Leu Glu Gly Gln Lys Asp			
153		290	295	300
154	Gly Phe Tyr Leu Tyr Pro Asp Gly Lys Thr His Asn Pro Asp Leu Thr			
155		305	310	315
156	Glu Leu Gly Gln Ala Glu Pro Gln Gln Arg Ile His Val Ser Glu Glu			
157		325	330	335
158	Gln Leu Gln Leu Tyr Trp Ala Met Asp Ser Thr Phe Glu Leu Cys Lys			
159		340	345	350
160	Ile Cys Ala Glu Ser Asn Lys Asp Val Lys Ile Glu Pro Cys Gly His			
161		355	360	365
162	Leu Leu Cys Ser Cys Cys Leu Ala Ala Trp Gln His Ser Asp Ser Gln			
163		370	375	380
164	Thr Cys Pro Phe Cys Arg Cys Glu Ile Lys Gly Trp Glu Ala Val Ser			
165		385	390	395
166	Ile Tyr Gln Phe His Gly Gln Ala Thr Ala Glu Asp Ser Gly Asn Ser			
167		405	410	415
168	Ser Asp Gln Glu Gly Arg Glu Leu Glu Leu Gly Gln Val Pro Leu Ser			
169		420	425	430
170	Ala Pro Pro Leu Pro Pro Arg Pro Asp Leu Pro Pro Arg Lys Pro Arg			
171		435	440	445
172	Asn Ala Gln Pro Lys Val Arg Leu Leu Lys Gly Asn Ser Pro Pro Ala			
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<213> ORGANISM: Homo Sapiens

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183	cccccttcgc	tgccggacct	gctgccccgc	acagcgcagc	tgcttcgaga	ggtggcccat	180
184	tctcggcggg	cggccggcgg	aggcggcccc	gggggtcccg	gcggctctgg	ggactttcta	240
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186	cggggccgaa	ggagtgccaa	cgacgagctc	ttccgggcgg	gctccagact	caggcgacag	360
187	ctggccaagc	tggccatcat	cttcagccac	atgcacgcag	agctgcacgc	actcttcccc	420
188	ggggcaaagt	actgtggaca	catgtaccag	ctcaccaagg	ccccgcacca	caccttctgg	480
189	agggaagt	gcggagcccc	gtgtgtgctg	ccctgggctg	agtttgagtc	cctcctgggc	540
190	acctgccacc	ctgtggaacc	aggctgcaca	gccctggcct	tgcgcaccac	cattgacctc	600
191	acctgcagcg	ggcacgtgtc	catcttcgag	ttcgacgtct	tcaccaggct	ctttcagcca	660
192	tggccaacac	tcctcaagaa	ctggcagctc	ctggcagtc	accacccagg	ctacatggcc	720
193	ttcctcacct	atgatgaggt	ccaagagcgt	ctgcaggcct	gcagggacaa	gccaggcagt	780
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DATE: 11/18/1999
TIME: 14:43:39

Input Set: I434708.RAW

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197	gagctcggcc	aggcagaacc	ccagcagcgc	atccacgtgt	cagaggagca	gctgcagctc	1020
198	tactgggcca	tggactccac	atttgagctc	tgcaagatct	gtgctgagag	caacaaggat	1080
199	gtgaagattg	agccgtgcgg	gcacctgctc	tgcaagatct	gctggtgctc	ctggcagcac	1140
200	tgggacagcc	agacctgccc	cttctgccgc	tgcgagatca	agggctggga	ggccgtgagt	1200
201	atctaccagt	tccacggtca	ggctactgct	gaggactcag	ggaacagcag	tgaccaggaa	1260
202	ggcagggagt	tggagctggg	gcaggtgccc	ctttcggctc	ctccattgcc	cccacggcca	1320
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214	tccaactccc	tgcttctctg	gtcactgctg	ttccctgagt	cctcagcagt	agcctgaccg	300
215	tagaactggt	agatactcac	ggcctcccag	cccttgatct	cgcagcggca	gaaggggcag	360
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225	tcccaggtgc	tcttgagggg	acagaaggac	ggcttctacc	tctaccaga	tggaaagacc	180
226	cacaacccag	acctgactga	gctcggccag	gcagaacccc	agcagcgcag	ccacgtgtca	240
227	gaggagcagc	tgagctctca	ctggggccatg	gactccacat	ttgagctctg	caagatctgt	300
228	gctgagagca	acaaggatgt	gaagattgag	ccgtgcgggc	acctgctctg	cagctgctgc	360
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238	gacctgacgg	agctctgcgt	aacgggaccc	tatcaacgca	tccacgtgtc	ggaggagcag	180
239	ctgcagctgt	actgggccat	gaactccaca	tacgagctct	gcaagatctg	tgccgagaga	240
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Input Set: I434708.RAW

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212	W "N" or "Xaa" used: Feature required	cgcangangn gggagttccc ctttaggagt ctcacttt
213	W "N" or "Xaa" used: Feature required	ctggggggca gatctggccg tgggggcaat ggaggagc
216	W "N" or "Xaa" used: Feature required	gtctgggctg tccgagtgt gccaggcanc caggcagc
223	W "N" or "Xaa" used: Feature required	agggacaagc caggcagtta catcttccgg cccagctg
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241	W "N" or "Xaa" used: Feature required	cctggcagaa ctcagacagn ccagacctgc ccttttct
242	W "N" or "Xaa" used: Feature required	ccagagcctg tgngttntcc atcagtttcc angggang
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